UNITED STATES DISTRICT COURT
SOUTHERN DISTRICT OF NEW YORK
----------X

UNITED STATES OF AMERICA,

Dkt. No. 15-CR-095 (AJN)

v.

DOMINICK SHERLAND,

Defendant.

----------X

MEMORANDUM OF LAW IN SUPPORT OF DEFENDANT DOMINICK SHERLAND'S MOTION TO EXCLUDE EVIDENCE GENERATED BY USE OF THE FORENSIC STATISTICAL TOOL AND REQUEST FOR A DAUBERT HEARING

Edward V. Sapone, Esq.
Chase Ruddy, Esq.
Sapone & Petrillo, LLP
One Penn Plaza, Suite 5315
New York, New York 10038
Telephone: (212) 349-9000

Todd Bussert, Esq.
Frost Bussert LLC
129 Church Street, Suite 226
New Haven, CT 06510
(203) 495-9790

TABLE OF CONTENTS

Page

Page

TABLE OF AUTHORITIES

Page(s)

Cases

Page(s)

Cases

Page(s)

Rules

Other Authorities

Page(s)

PRELIMINARY STATEMENT

The government is seeking to introduce, against Defendant Sherland at trial, the results of, and testimony regarding, DNA analyses conducted by the New York City Office of the Chief Medical Examiner ("OCME"), using the Forensic Statistical Tool ("FST").

FST is unreliable both generally and as applied to the facts of this case. FST was never generally accepted in the scientific community, as OCME was the *only* laboratory in the world to ever use it, and not even OCME is using it anymore. The FST's unique system of fixed parameters fails to account for the specific features of real world crime-scene samples, including those present in this case, which can increase the likelihood ratio ("LR"), prejudicing the defendant. The source code has shown that FST is something different than what it has been made out to be, which has clear implications for the reliability of FST, especially given that FST as it currently exists has never been vetted by any expert outside of OCME. And, it has not been subjected to adequate peer review.

Any one of these issues should bar FST's admission against a criminal defendant at trial, as the LR is uniquely open to bias and unfair prejudice. When viewed together, FST's record reflects such an utter disregard of sound methodology that it even undermines the relevance of FST's results. For all of these reasons, we seek the exclusion of all evidence generated by, and testimony concerning, FST, or in the alternative, request a *Daubert* hearing. *See Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579 (1993).

By way of background, on April 12, 2016, a grand jury returned an indictment charging Mr. Sherland and 63 co-defendants with RICO, narcotics offenses, and use of a firearm in furtherance of the racketeering enterprise and narcotics conspiracy. (*See* S2 indictment, ECF Docket Entry "DE" 97).

According to the government, the defendants were members and associates of the Big Money Bosses street gang ("BMB") operating in the northeast Bronx. The government alleges that BMB members and their associates engaged in shootings and other acts of violence against rival Bronx gangs, including: (a) the "2Fly YGz," a gang based in the Eastchester Gardens housing project; (b) the "Slut Gang," based in the Boston Secor projects; and (c) the "YSGz," based in the Edenwald Houses.

On July 6, 2017, the grand jury returned a superseding indictment (S6-15 Cr. 95) charging Mr. Sherland with additional offenses including murder in aid of racketeering and an additional firearm offense.

The focus of this motion is the DNA evidence which the government will seek to admit in support of the murder in aid of racketeering charge.

According to the government, Mr. Sherland stabbed and killed Jeffrey Delmore to further the objectives of BMB. (*See* S6 indictment, ECF DE 1502).

More specifically, the Government alleges in its September 17, 2016 Enterprise Letter:

> On or about May 15, 2010, in the vicinity of Gunhill Road in the Bronx, DOMINICK SHERLAND, GERARD BASS, MARLON ROBERTS, BARFFOUR ABEBERSE, MASHUD YODA, STEPHAN CLARKE, JOSE RODRIGUEZ, BRIAN RICHARDS, ANTHONY KING, ANDERSON ROSS, MICHELLE JEMISON and others chased a group of people including Jeffrey Delmore. SHERLAND, BASS, YODA, RODRIGUEZ, ROBERTS, and others caught up with Delmore and began to kick and beat him, and SHERLAND stabbed Delmore with a knife, from which Delmore later died.

The government's anticipated evidence of Mr. Sherland's participation in the murder of Jeffrey Delmore is principally twofold: (1) the testimony of cooperating witnesses, and (2) the results of DNA analyses generated by FST.

The FST is a proprietary software program that was developed by the OCME. As I am sure this Court is aware, FST assigns a statistical weight, or likelihood ratio ("LR"), to DNA

mixtures that cannot be "deconvoluted" or separated into individual profiles. A LR reports a statistical association between the DNA evidence and an individual suspect. There are other LR programs, both online and in development. But the FST's methodology is unique in that it utilizes a system of fixed parameters, tied to DNA quantity, for calculating the LR in all cases. Other programs, including the STR Mix program, permit customization of the parameters to the specific evidence in a case. By January 1, 2017, the OCME had abandoned the FST in favor of the STR Mix program.

The OCME used the FST to compare Mr. Sherland's DNA profile with DNA mixtures extracted from the thin sides, and the handle, of a knife alleged to be the murder weapon used to stab Delmore on May 15, 2010.

Based on its analysis, the OCME concluded that (1) both mixtures contained the DNA of three people, (2) it "is approximately 4,070 times more probable if the sample [on the thin sides of the knife handle] originated from Dominick Sherland and two unknown, unrelated persons than if it originated from three unknown, unrelated persons," (3) the LR of 4,070 provides "very strong support" that Dominick Sherland and two unknown, unrelated persons contributed to the mixture, (4) it "is approximately 4.59 times more probable if the sample [on the knife handle] originated from Dominick Sherland and two unknown, unrelated persons than if it originated from three unknown, unrelated persons," and (5) the LR of 4.59 provides "limited support" that Dominick Sherland and two unknown, unrelated persons contributed to the mixture. *See* Exhibit A.

Given the Court's role, at the intersection of science and the law, when dealing with scientific evidence, the court must determine whether the evidence is sufficiently relevant and reliable to be heard by a jury. The OCME's own validation studies for the FST, the scientific

literature, Dr. Eli Shapiro's expert declaration, and the prior testimony of esteemed scientific experts all demonstrate that the FST is unreliable and should not be used in court.

There are several core problems with FST. Most critically, FST's unique system of fixed parameters fails to account for the specific features of real world crime-scene samples and can have the effect of making the LR higher, thereby prejudicing a criminal defendant.

Second, recent revelations, since the source code was made available, have shown that FST is performing "undocumented behavior," including functions that do not reflect, and are even counter to, the methodology as described by the OCME in prior testimony before judges in court cases, and in affidavits submitted in connection with past litigation involving FST. The fact that FST is something different than what it has been made out to be has clear implications for the reliability of FST. It can presently be said with certainty that (1) the OCME never made clear that its flagship, copyrighted software differed in any way from its documentation; (2) the issue is significant as even small changes to a locus LR are shown to affect the conclusions in OCME reports; and (3) the FST authors' omission of this hidden function from any documentation, validation, testimony, or any other opportunity already afforded them to identify and explain it severely damages what credibility they may retain.

Further, the FST is not generally accepted in the scientific community, as the OCME was the *only* laboratory in the world to use it, and the OCME is not even using it anymore, having abandoned it in favor of the STR Mix program. In addition, the FST has not been subjected to adequate peer review. Validation must be by groups independent of those who developed a technique, and multiple groups should be able to validate a program before it should be considered acceptable to the scientific community.[1] That was not the case with the FST. The

[1] *See* Opinion by Justice Mark Dwyer in the combined cases of *People v. Thompson, Jackson & Seepersad*, N.Y. County, Oct. 16, 2017 (Ind. Nos. 4346/15, 1644/16, and 2939/16) (attached as Exhibit

FST was validated by its developer only. Further, the source code was published online only five months ago, well after the OCME stopped using the FST on January 1, 2017, which reduces the interest in the scientific community in deciding whether FST works. Even apart from that, much of the key data used to develop the FST has not been preserved or made available for inspection by the scientific community. These flaws further render the FST unreliable under *Daubert.*

While not dispositive of the issues presented here, notably the admission of FST evidence has not been widely accepted by other courts. To our knowledge, FST evidence has only ever been used in a federal criminal trial over a defendant's objection on one occasion: *United States v. Dean Jones* (15-CR-153 (VSB))[2]. Meanwhile, New York State courts are split. In October 2013, a Supreme Court judge in New York County admitted FST evidence in a criminal case following an evidentiary hearing. *People v. Rodriguez,* Sup Ct, NY County, Oct. 24, 2013, Caruthers J., Ind. No. 5471-2009.[3] In November 2014, however, a second Supreme Court judge in Kings County excluded the introduction of FST evidence in the combined cases of *People v. Peaks & Collins*, Sup Ct, Kings County, Nov. 7, 2014, Dwyer, J., Ind. Nos. 80077-2010, 7690-2010. *See* Exhibit D. The court found that at that time that there was no "general agreement in the scientific community as to the challenged scientific principles." *Id.* at 4. Subsequently, in

---

B); *see also* Report To The President Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods, President's Council of Advisors on Science and Technology (September 2016) (attached as Exhibit C).

[2] Judge Broderick, in a two-page order, dated November 30, 2017, found that the methods of FST testing utilized by the OCME in that case were sufficiently reliable to satisfy the *Daubert* standard, but to date, no opinion setting forth the Court's findings and reasoning for that decision has been issued.

[3] Some New York courts have also admitted FST evidence without holding a *Frye* hearing. *See, e.g.*, *People v. Garcia*, 39 Misc.3d 482 (Sup Ct, Bronx County 2013); *People v. Styles*, 40 Misc.3d 1205(A), 2013 N.Y. Slip Op. 51019(U), *2-3 (Sup Ct, NY County 2013); *People v. Horne*, Ind. No. 1647/2015, Sup Ct. Bronx Co. January 21, 2017; *People v. Lopez*, 50 Misc.3d 632 (Sup. Ct. Bronx Co. 2015); *People v. Belle*, 47 Misc.3d 1218(a) (Sup. Ct. Bronx Co. 2015). These decisions are of limited force, however, because the defense was not permitted to introduce expert testimony to counter the prosecution's claims.

October 2017, Justice Dwyer, now sitting in New York County, excluded the introduction of FST evidence in the combined cases of *People v. Thompson, Jackson and Seepersad*, (N.Y. County, Oct. 16, 2017, Ind. Nos. 4346/15, 1644/16, and 2939/16), finding that "there hasn't been enough of a change since mid-2015 that shows a new consensus in the field that has developed as to the FST." Exhibit B at 5. And, in *People v. Shamoy Brown* (Ind. No. 0330/2016, Sup. Ct. Bronx Co.), the Honorable Ralph Fabrizio, who had previously admitted FST evidence, recently acknowledged the renewed need for a *Frye* hearing.[4] He ordered the *Frye* hearing to address the newly disclosed information that OCME changed and modified FST after FST's validation studies and the application for approving its use in casework was submitted, and agreed to, by New York State -- something that had not previously been addressed by any of the New York State cases admitting FST evidence. *See* Exhibit E at 4-5.

Therefore, given the very limited acceptance of FST, and the issues raised by this motion, we ask that the Court, in exercising its essential gatekeeper function, grant our request for a *Daubert* hearing and ultimately exclude the government's DNA evidence. Simply put, OCME's discontinued FST methodology is unreliable under *Daubert*, and the admission at trial of any evidence produced by this unreliable methodology would be unfairly prejudicial and would confuse and mislead the jury.

[4] *See* Opinion by Justice Ralph Fabrizio in *People v. Shamoy Brown* (Ind. No. 0330/2016, Sup. Ct. Bronx Co.) (attached as Exhibit E). Judge Fabrizio delayed the *Frye* hearing until the conclusion of a pending investigation by the New York State Inspector General, as the allegations raised before the Inspector General could have potential penal implications for individuals who might be required to testify at the *Frye* hearing. *See id*. at 6.

FACTUAL BACKGROUND

A.

The Alleged Offense

On May 15, 2010, at approximately 11:40 p.m., in the vicinity of East Gun Hill Road and Fish Avenue in the Bronx, Jeffrey Delmore was stabbed once in the chest and ran approximately two blocks to 3055 Bouck Avenue where he collapsed in the building lobby. He was subsequently transported to Jacobi Hospital where he died at approximately 2:07 a.m.

Later that night, officers recovered from the vicinity of East Gun Hill Road and Fish Avenue, several items, including a black-handled steak knife, which was submitted for DNA analysis to identify potential suspects. *See* Exhibit F.

No arrests were made. It was only after Mr. Sherland was arrested in this case, and after other defendants entered into cooperation agreements with the government, pursuant to which they provided information to the government about the alleged circumstances surrounding the stabbing, that the government obtained a superceding indictment against Mr. Sherland charging him with Delmore's murder.

B.

The DNA Evidence and Analysis

The government intends to introduce DNA evidence allegedly connecting Mr. Sherland to the knife used in the stabbing. Following the filing of the S6 superceding indictment on July 5, 2017, the government was granted a search warrant authorizing a DNA sample from Mr. Sherland. The OCME then compared Mr. Sherland's DNA sample to the DNA recovered from the knife. The OCME analyzed the DNA evidence using traditional PCR/STR testing and the

FST. That analysis yielded the conclusions, including the LRs referenced above, that are the subject of this motion.

1. Traditional PCR/STR DNA Analysis

DNA (deoxyribonucleic acid) is the hereditary material found inside all human beings. *See* Declaration of Dr. Eli Shapiro ("Shapiro Decl.") ¶ 11. It is frequently referred to as our "genetic blueprint." *Id.* DNA is located in every nucleated cell in the body. *Id.* No two individuals, with the exception of identical twins, have the same genetic code. *Id.* A chromosome is the tightly packaged structure of DNA. *Id.* at ¶ 12. Each nucleated human cell contains 22 pairs of chromosomes; one chromosome from each pair is inherited from a person's father, and the other comes from the person's mother. *Id.* There is also a 23rd pair, which is called the sex chromosome, X and Y. *Id.*

Most modern forensic analyses look at Short Tandem Repeats ("STRs"), which are small segments of DNA that are repeated in tandem. *See id.* at ¶ 13. STRs are distributed among each person's DNA at specific locations ("loci"). *Id.* An allele is a number that describes the size of the DNA fragment, or the number of repeats of the STR motif, at a location ("locus"). *See id.* at ¶ 14. Every person has two alleles at each locus—one inherited from the mother and one from the father. *Id.* If the two alleles at a locus are different, they are known as "heterozygous." *Id.* If they are the same, then they are "homozygous." *Id.*

In this case, 15 core loci were examined; now, laboratories are testing seven additional loci. *Id.* at ¶ 15. One number is reported for each allele at a locus. *Id.* For example, if one chromosome has 13 repeats of the STR motif and the other has 18 repeats, the result is reported as 13, 18 for the particular locus. *Id.* An individual DNA profile is, thus, a string of numbers representing the alleles at each of the loci examined. *Id.* Although many individuals will share a

particular allele at a particular locus, the chance that two people will have the same set of alleles at multiple loci decreases as the number of examined loci increases. *Id.* Thus, an analyst can use the observed allele combinations at multiple loci to distinguish one individual from another. *Id.* Decreasing the number of loci used to calculate a statistical weight of DNA evidence decreases the discriminatory power of the evidence, and increases the chances of false positive associations. *See id*.

Basic forensic DNA analysis involves several steps. First, DNA is extracted from the evidence. *Id.* at ¶16; *see also* National Institute for Justice, "DNA for the Defense Bar" (June 2012), at 12, *available at* https://www.ncjrs.gov/pdffiles1/nij/237975.pdf. At the second step, quantification, the analyst measures the amount of DNA present in the sample. *See* Shapiro Decl. ¶ 16. The third step is amplification, in which a process called polymerase chain reaction ("PCR") is applied to the DNA sample. *Id.* PCR makes millions of copies of a particular segment of DNA so that it can be detected and analyzed. *Id.* In the fourth step, a process known as electrophoresis separates the STR fragments by size. *Id.* The data from the electrophoresis then becomes the input for a software program—in this case Genemapper—that converts the data to graphs, which can be formed and presented in a number of ways. *Id.* The labeling and graphs produced by the Genemapper program are called electropherograms. *Id.* Electropherograms contain differing peak heights at the different allelic positions. Once an electropherogram is generated, the analyst reviews it, draws conclusions about the DNA sample, and creates a DNA profile. *Id.* at ¶17. In the final step, the analyst compares the profile created with the suspect's DNA profile. *Id.*

2. DNA Mixtures

A DNA mixture is a sample containing the DNA of two or more individual contributors. Shapiro Decl. ¶ 18. DNA mixtures cannot be easily "deconvoluted" or separated into individual profiles. *Id.* at ¶ 19. In addition, while the quantification step described above provides an estimate as to the total amount of DNA in a mixture, the quantity of DNA from each individual contributor remains unknown, irrespective of the accuracy of the quantification process. *Id.*

3. Drop-Out and Drop-In

The process of PCR can result in random errors or "stochastic effects." *See* Shapiro Decl. ¶ 22. Two of the most common errors are allele drop-out and allele drop-in. *Id.* Drop-out occurs when alleles from the principal donors to a DNA mixture fail to appear in the profile. *Id.* Drop-in occurs when alleles not originating from the principal donors to a mixture show up in a DNA profile. *Id.*

Drop-out can also result from degradation. *Id.* at ¶ 23. Dirt, bacteria, and sunlight can all cause DNA degradation. *Id*. Touched DNA is also frequently degraded. *Id.* DNA varies by length, and longer pieces of DNA will break down faster than shorter pieces. That means, when DNA is degraded, some longer pieces of DNA may not be detected. *Id.*

A third reason for drop-out involves the relative proportions of DNA in a DNA mixture. *Id.* at ¶ 24. If the amount of DNA from each contributor is not even, more pieces of one donor's DNA might be grabbed during sampling or electrophoresis. Therefore, some alleles will not be detected. *Id.*

As discussed more fully below, the accurate calculations of allele drop-out and drop-in are critical to the successful operation of any LR program, including FST.

4. FST

FST is a proprietary software program developed by the New York OCME. The program examines the alleles found in DNA mixtures that cannot be deconvoluted; then it determines a statistical weight, or likelihood ratio ("LR"), that the suspect's DNA is included in the mixture. *Id.* at ¶ 25. According to the OCME, the "LR value provides a statistical measurement of the strength of support for one scenario over another, i.e., one scenario being that a known person contributed to a mixture versus the scenario that an unknown, unrelated person contributed instead." NYC Office of Chief Medical Examiner, *Forensic Biology Protocols for Forensic STR Analysis* at 440 (hereafter "OCME Forensic STR Analysis Protocol")(attached as Exhibit G). The numerator of the LR calculates the conditional probability using the assumptions of the prosecution scenario (which includes the defendant), while the denominator calculates a conditional probability assuming the defense scenario (which excludes the defendant). *See* Shapiro Decl. ¶ 25.

The FST's methodology is unique in that it utilizes pre-determined allele drop-out and drop-in rates based on DNA quantity to determine the LR. *Id.* at ¶ 32. *See also* Exhibit D to Shapiro Decl., Adele A. Mitchell et al., *Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in*, Forensic Sci. Int'l: Genetics 6 749-761, 756 (2012) (hereafter "*FST Validation Study*") ("The drop-out rate estimates employed by FST depend on DNA template quantity.") This methodology is discussed in detail in below. OCME is the only laboratory in the world to calculate the drop-out rate based on DNA quantity.

In addition to calculating the LR, the OCME also offers an interpretation of the strength or weakness of its calculation. OCME's qualitative interpretations report LR values in accordance with the following table, which the OCME made up:

Reported Value	Qualitative Interpretation
Less than 0.001	Very strong support for Defense Hypothesis over Prosecution Hypothesis
0.001 to 0.01	Strong support for Defense Hypothesis over Prosecution Hypothesis
0.01 to 0.1	Moderate support for Defense Hypothesis over Prosecution Hypothesis
0.1 to 1	Limited support for Defense Hypothesis over Prosecution Hypothesis
1	No conclusions
1 to 10	Limited Support for Prosecution Hypothesis over Defense Hypothesis
10 to 100	Moderate Support for Prosecution Hypothesis over Defense Hypothesis
100 to 1000	Strong Support for Prosecution Hypothesis over Defense Hypothesis
Greater than 1000	Very Strong Support for Prosecution Hypothesis over Defense Hypothesis

See Exhibit G, OCME Forensic STR Analysis Protocol at 467. Thus, for any LR greater than one, OCME concludes that there is at least some support for the prosecution hypothesis, i.e. that the suspect's DNA is included in the mixture. When the LR value is less than one, the OCME concludes that the mixture is better explained by the defense hypothesis. *See id.*

The OCME began work on the development of the FST in 2008. Theresa Caragine, Ph.D. and Adele Mitchell, Ph.D., headed the group within the OCME who developed and validated the program. *See e.g.*, Investigation into the New York City Office of Chief Medical Examiner: Department of Forensics and Biology, State of New York, Office of the Inspector General 28 (Dec. 2013), *available at* http://ig.ny.gov/pdfs/OCMEFinalReport.pdf. (noting that "In 2008, Adele Mitchell, a statistician, was hired to assist in developing the software, eventually known as the FST. Caragine was also instrumental in creating the FST") (hereafter "Inspector General

Report");[5] *see also* Exhibit D to Shapiro Decl., *FST Validation Study* at 759; Exhibit F to Shapiro Decl., Jaheida Perez, *et al*., *Estimating the number of contributors to two-, three-, and four-person mixtures containing DNA in high template and low template amounts*, Croat. Med. J. 52, 314-26, 314 (2011) (hereafter "*Perez Study*") (listing Mitchell and Caragine as authors).

In 2010, the DNA Subcommittee to the New York State Commission on Forensic Science issued a recommendation approving the use of FST in forensic cases. The Commission then adopted the subcommittee's recommendation. The OCME then began using FST in its criminal casework. *See* Exhibit D to Shapiro Decl., *FST Validation Study* at 759. Notably, OCME did not provide the DNA Subcommittee with the actual FST program or with the source code for the FST prior to requesting its approval.

Validations are the process by which labs demonstrate that their methods are robust and reliable. Following the DNA Subcommittee's approval of the FST, in 2011 and 2012, the OCME published two articles outlining the results of its validation studies on the software – the FST Validation Study and the Perez Study. *See* Exhibit D to Shapiro Decl., *FST Validation Study*; Exhibit F to Shapiro Decl., *Perez Study*. The FST was never vetted, however, by anyone outside of OCME's own staff.

Importantly, after approval by the relevant New York State officials, and after the validation, a software glitch was discovered within FST. OCME brought in an outside contractor to fix the software, and while fixing the software, they made other modifications as well. OCME failed to inform the Committee, or anyone else of the changes. There was no new validation, and

[5] Dr. Caragine is a former Deputy Director of the Department of Forensic Biology within the OCME. *See* Inspector General Report, at 26. On April 19, 2013, Dr. Caragine resigned her position for allegedly failing to follow lab protocol, which prompted an investigation by the State of New York, Office of the Inspector General. *Id.* at 26. After the investigation, the Office of the Inspector General issued a report, finding that "in two instances, [Dr. Caragine] ignored laboratory protocol regarding resolution of scientific disputes by rewriting a final report and reassigning cases when she disagreed with the findings rather than bringing them to the DNA technical leader for arbitration." *Id.* at 1.

given that FST is a black box, nobody else could look at it and discover that there had been a change or determine if there were any other software glitches of the same sort. *See* Exhibit B, Dwyer 2017 Opinion at 7-8. FST was not examined to even see if there should have been a new validation.

This continued to be the case until the Court in *United States v. Kevin Johnson* (15-CR-565 (VEC)), in July 2016, pursuant to a protective order, permitted the first outside review of FST's source code. That review revealed FST to be performing "undocumented behavior." That is, the code performed a routine that was not set forth in its documentation. Inside its black box, FST is something different than what it has been made out to be by its creators.

5. The August 2, 2017 OCME Report In This Case

The OCME issued its report on August 2, 2017, documenting its comparison, through FST, of Mr. Sherland's profile with the DNA evidence retrieved from (1) swab "RB/S2" from "thin sides of knife handle" and (2) sample from handle of knife. *See* Exhibit A. The OCME performed two electropherogram runs on each of the DNA mixtures. *See* Exhibit A. Tables charting OCME's comparison of the runs to Mr. Sherland's DNA profile are set forth below.

(1) Swab "RB/S2" from "thin sides of knife handle"

Profile	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317
Dominick Sherland	12, 15	31.2, 32.2	10, 11	11, 11	16, 17	7, 8	11, 13
Evidence							
Run 1	12, 13, 14, 15				14, 15, 16, 17	6, 7, 8	
Run 2	12, 13, 14, 15	31.2			14, 15, 16, 17	6, 7, 8, 9.3	11

Profile	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
Dominick Sherland	9, 9	22, 23	12, 13	14, 16	6, 8	13, 17	11, 13	21, 25
Evidence								
Run 1			12, 13	16				
Run 2	9		11, 12, 12.2, 13, 14, 16	14, 15, 16, 18, 20	6, 8		11, 12, 13	

(2) Sample from handle of knife

Profile	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317
Dominick Sherland	12, 15	31.2, 32.2	10, 11	11, 11	16, 17	7, 8	11, 13
Evidence							
Run 1	12, 14, 15, 16	29, 31, 32.2, 37	8, 10	11, 12	14, 15, 16, 17	6, 7, 8, 9.3	11, 12, 13
Run 2	12, 13, 14, 15	27, 29, 37	8, 10	11, 12	14, 15, 16, 17	6, 7, 8	11, 12, 13

Profile	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
Dominick Sherland	9, 9	22, 23	12, 13	14, 16	6, 8	13, 17	11, 13	21, 25
Evidence								
Run 1	8, 9, 11, 12, 13	17, 23	11, 12, 12.2, 13, 14, 15	14, 15, 16, 18, 20	6, 8, 9	13, 16, 17	11, 12, 13	21, 24
Run 2	9, 10, 11, 12	17, 22	11, 12, 12.2, 13, 14	14, 16, 17, 20	6, 8		11, 12, 13	19, 24

As demonstrated by the first table, the two runs, which are replicates from the same DNA extract, produced the same results at only 2 of the 15 loci examined because of allele drop-out and drop-in. *See* Shapiro Decl. ¶ 41. At Locus D19S433, for example, Run One identified two alleles, and Run Two identified six alleles. At 15 of the 30 loci examined in the two runs, no

alleles were present, indicating full drop-out at those loci. This provides an indication that the sample was severely degraded. *Id*.

Because the two runs showed different results, and because of the degradation, the OCME compared all of the alleles from both runs with Mr. Sherland's DNA profile. *Id*. ¶ 42.The analyst then ran FST and concluded that "[t]he DNA mixture found on 'swab RB/S2' from 'thin sides of knife handle' is approximately **4,070 times more probable** if the sample originated from Dominick Sherland and two unknown, unrelated persons, than if it originated from three unknown, unrelated persons. **Therefore, there is very strong support that Dominick Sherland and two unknown, unrelated persons contributed to the mixture, rather than three unknown, unrelated persons**." Exhibit A.

In the second table, where DNA typing of the sample provided results at 29 out of 30 loci, the two runs produced different results at 10 of the 15 loci examined, because of allele drop-out and drop-in. *See* Shapiro Decl. ¶ 49.At Locus D18S51, for example, Run One identified three alleles, and Run Two had total dropout. At D21S11, one of Mr. Sherland's alleles was present in Run One (32.2), but neither of his alleles was present in Run Two. At D2S1338, one of Mr. Sherland's alleles was present in Run One (23) which was not present in Run Two, while his other allele (22) was present in Run Two, but absent in Run One.

Because the two runs showed different results, OCME compared all of the alleles from both runs with Mr. Sherland's DNA profile. *Id*. ¶ 50. The analyst then ran the FST and concluded that "[t]he DNA mixture found on sample from handle of knife is approximately **4.59 times more probable** if the sample originated from Dominick Sherland and two unknown, unrelated persons, than if it originated from three unknown, unrelated persons. **Therefore, there**

is limited support that Dominick Sherland and two unknown, unrelated persons contributed to the mixture, rather than three unknown, unrelated persons." Exhibit A.

Mr. Sherland was excluded as a contributor to all other samples where comparisons could be made. *See* Exhibit A.

THE *DAUBERT* STANDARD

Federal Rule of Evidence 702 allows for the admissibility of expert testimony so long as "(1) the testimony is based upon sufficient facts or data, (2) the testimony is the product of reliable principles and methods, and (3) the expert has applied the principles and methods reliably to the facts of the case." Fed. R. Evid. 702. The district court is charged with "ensur[ing] that any and all scientific testimony or evidence admitted is not only relevant, but reliable." *Daubert*, 509 U.S. at 589.

As part of its gatekeeping function under FRE 702, the court must make a "preliminary assessment of whether the reasoning or methodology underlying the testimony is scientifically valid and of whether that reasoning or methodology properly can be applied to the facts in issue." *Daubert*, 509 U.S. at 592-93. The Supreme Court has identified a number of factors bearing on reliability that district courts may consider, such as: (1) whether a theory or technique "can be (and has been) tested;" (2) whether the theory or technique "has been subjected to peer review and publication;" (3) a technique's "known or potential rate of error;" and the "existence and maintenance of standards controlling the technique's operation;" and (4) whether a particular technique or theory has gained "general acceptance" in the "relevant scientific community." *Id.* at 593-94; *see also Amorgianos v. Nat'l R.R. Passenger Corp.*, 303 F.3d 256, 266 (2d. Cir. 2002).

These factors are not a "definitive checklist or test." *Daubert*, 509 U.S. at 594. Rather, the *Daubert* inquiry is "fluid" and "will necessarily vary from case-to-case." *Amorgianos*, 303 F.3d at 266. The Court has "considerable leeway" in "deciding how to test an expert's reliability, and to decide whether or when special briefing or other proceedings are needed to investigate reliability." *Kumho Tire Co. v. Carmichael*, 526 U.S. 137, 152 (1999).

"To warrant admissibility…it is critical that an expert's analysis be reliable at every step." *Amorgianos*, 303 F.3d at 267. Further, an expert's conclusions must be "supported by good grounds for *each step* in the analysis" and "*any* step that renders the analysis unreliable under the *Daubert* factors renders the expert's testimony inadmissible." *Id.* at 267 (internal citations and quotations omitted) (emphasis added); *see also Heller v. Shaw Indus., Inc.*, 167 F.3d 146, 155 (3d Cir. 1999) ("[T]he reliability analysis applies to all aspects of an expert's testimony: the methodology, the facts underlying the expert's opinion, the link between the facts and the conclusion, *et alia*.")

Thus, "when an expert opinion is based on data, a methodology, or studies that are simply inadequate to support the conclusions reached, *Daubert* and FRE 702 mandate the exclusion of that unreliable opinion testimony." *Amorgianos*, 303 F.3d at 266. The same is true when a reliable methodology is changed or misapplied in a particular case. *See In re Paoli R.R. Yard PCB Litig.*, 35 F.3d 717, 745 (3d Cir. 1994) ("any step that renders the analysis unreliable under the *Daubert* factors renders the expert's testimony inadmissible. This is true whether the step completely changes a reliable methodology or misapplies that methodology.")

In addition, while the thrust of the *Daubert* inquiry is on scientific methodology, the conclusions drawn by the expert are also relevant. The Supreme Court has stated: "[C]onclusions and methodology are not entirely distinct from one another….[N]othing in either *Daubert* or the

Federal Rules of Evidence requires a district court to admit opinion evidence that is connected to existing data only by the *ipse dixit* of the expert. A court may conclude that there is simply too great an analytical gap between the data and the opinion proffered." *General Electric Co. v. Joiner*, 522 U.S. 136, 146 (1997).

Finally, in assessing the admissibility of expert evidence, a district court should be mindful of other applicable rules, including Federal Rule of Evidence 403, which permits the exclusion of evidence if its "probative value is substantially outweighed by the danger of…unfair prejudice, confusion of the issues, or misleading the jury…." *Daubert*, 509 U.S. at 595; Fed. R. Evid. 403. Courts have noted the potential "mystic infallibility" of scientific evidence, particularly DNA evidence. *United States v. Williams*, 583 F.2d 1194, 1199-1200 (2d Cir. 1978), *cert. denied*, 439 U.S. 1117 (1978). *See also United States v. Jakobetz*, 747 F.Supp. 250, 262 (D. Vt. 1990) ("Arguably, DNA profiling is particularly capable—in more ways than one—of lulling a jury into slumbering at its post and not rigorously sifting the evidence.") Because "[e]xpert evidence can be both powerful and quite misleading … the judge in weighing possible prejudice against probative force under Rule 403...exercises more control over experts than over lay witnesses." *Daubert*, 509 U.S. at 595. (citation omitted).

As the proponent of the expert evidence, the government bears the initial burden of proving reliability and relevance by a fair preponderance of the evidence. *Liberty Media Corp. v. Vivendi Universal*, 874 F.Supp. 2d 169, 172 (SDNY 2012). The government cannot meet its burden here.

ARGUMENT

Traditional single source DNA typing has become a mainstay of forensic science. Hundreds of law enforcement laboratories in the United States utilize standard STR/PCR DNA testing in criminal cases, and both state and federal courts universally recognize the reliability of STR/PCR DNA testing and admit the results.

The statistical evaluation of DNA mixtures, by contrast, is a relatively new field, and the forensic DNA community is still trying to pave a path forward. In recent years, various software programs have emerged for computing LRs with DNA mixtures. These programs are each in differing stages of development; they each employ a different statistical model; and they each generate differing results. *See* Exhibit H, Christopher D. Steele and David J. Balding, *Statistical Evaluation of Forensic DNA Profile Evidence*, Annu. Rev. Stat. Appl. 2014, 1:361-84, at 381 (hereafter "*Statistical Evaluation*"); *see also* Exhibit C to Shapiro Decl., Hinda Haned, et al., *Complex. DNA mixture analysis in a forensic context: Evaluating the probative value using a likelihood ratio model*, Forensic Sci. Int'l: Genetics 16, 17-25, 17 (2015) (hereafter "*Complex. DNA mixture analysis*")("In recent years … a number of new computer programs have been introduced. These software are anchored in a likelihood-ratio model, but they all use different probabilistic models, and rely on different distributional assumptions."); Exhibit I, Steven P. Lund and Hari Iyer, *Likelihood Ratio as Weight of Forensic Evidence: A Closer Look*, J. of Research of Natl. Inst. of Standards and Tech., Vol. 122, Art. No. 27 (2017).

The OCME is the *only* laboratory in the world that utilized the FST, and as mentioned, they no longer employ the FST. The methodology underlying the FST is unique, and its reliability is a disputed topic in the scientific community and in courtrooms across New York.

In 2014, in *People v. Peaks & Collins*, two combined criminal cases in Kings County Supreme Court, the Hon. Mark Dwyer excluded the introduction of FST evidence finding that the program has not been generally accepted in the scientific community. *See* Exhibit D at 6 ("the dissenting chorus was strong enough that I can't say that the *Frye* test has been satisfied.") The Court's decision followed an extensive evidentiary hearing, which took place over the course of a year and included testimony from 11 experts. More recently, in October 2017, Justice Dwyer confirmed his earlier decision in an oral opinion in the combined cases of *People v. Thompson, Jackson & Seepersad*, (N.Y. County, Oct. 16, 2017, Ind. Nos. 4346/15, 1644/16, and 2939/16), finding that "there hasn't been enough of a change since mid-2015 that shows a new consensus in the field that has developed as to the FST." Exhibit B.

The only state court to have admitted the FST following an evidentiary hearing, *see People v. Rodriguez,* Sup Ct, NY County, Oct. 24, 2013, Caruthers, J., Ind. No. 5471-2009, found that likelihood ratios "have long been generally accepted by forensic scientists as reliable." This may be true, but the Court's reasoning in *Rodriguez* is nonetheless flawed.

The primary question is not whether likelihood ratios are accepted in other settings. The question is whether the OCME's application of a likelihood ratio here—using pre-set drop-out and drop-in rates—is reliable and generally accepted by the relevant scientific community. *See Paoli,* 35 F.3d at 745 ("any step that renders the analysis unreliable under the *Daubert* factors renders the expert's testimony inadmissible. This is true whether the step completely changes a reliable methodology or misapplies that methodology"); *See also* Exhibit J, Hinda Haned, et al., *Exploratory data analysis for the interpretation of low template DNA mixtures,* Forensic Sci. Int'l: Genetics 6, 762-74, 773 (2012) (hereafter "*Exploratory data analysis*") ("likelihood ratios rely on the model used to generate them"). The answer to this question is no.

Given that the FST's final LR depends on the assumed number of contributors, the drop-out values, and drop-in values, being input into the calculation, errors associated with these estimated parameters directly impact the reliability and general acceptance of FST. As discussed below, the errors are numerous. Each error, and certainly their combined effect, renders the FST inadmissible under *Daubert*.

A.

Because The FST Methodology Used to Develop the Drop-Out Rate is Flawed, FST's Results Are Unreliable

1. Using DNA Quantity to Determine the Drop-Out Rates Has Never Been Done Before and is Unproven

The FST's methodology was unique in that it utilized pre-determined allele drop-out and drop-in rates based on DNA quantitation. The OCME's main assumption was that the drop-out and drop-in rates may be determined based on the amount of DNA in a sample. *See* Exhibit D to Shapiro Decl., *FST Validation Study* at 756. No other lab or program in the world ascribes to this hypothesis. *See* Exhibit K, Testimony of Dr. Eli Shapiro, *People v. Peaks & Collins,* 10/15/2013, at 177 ("Yes, I think the entire approach of the FST, which is a very unique one, and I think the only one in the field, is to use the quantitation values, for a sample, in order to determine the drop-out rates to apply to the mixture."); *see also* Exhibit L, Testimony of Dr. Bruce Budowle, *People v. Peaks & Collins,*12/9/2013, at793 (The FST "makes certain assumptions about DNA typing that no one else would do even in all standard DNA typing. The

main assumption being made is that all the rates for drop-in, drop-out are based on the amount of the DNA….")[6].

There are various competing LR ratio programs, including *STR Mix, LoComatioN, Forensim, TrueAllele, likeLTD, Armed Xpert,* and *LabRetreiver*. Unlike the FST, however, none of these programs arrives at pre-determined drop-out rates based on DNA quantity. Rather, they allow the user to input a range of drop-out rates based on the specific features of a case, or they focus on the average peak heights at the allelic positions.[7] In short, each of these programs rejects the FST's pre-set drop-out methodology. *See e.g.*, Exhibit N, David J. Balding and John Buckelton, *Interpreting low template DNA profiles*, Forensic Sci. Int'l: Genetics 4,1-10 (2008)(creators of likeLTD arguing that "DNA-based prosecutions that rely on drop-out and do not explicitly estimate plausible ranges for the drop-out rate parameter, are in our view, defective."); Exhibit J, *Exploratory data analysis* at 768 (creators of Forensim suggesting the use of a range of drop-out rates based on the crime scene sample itself with the advantage being "that the ranges of the drop-out probability can be evaluated separately under Hp and Hd, and that we avoid reporting values of drop-out that are supported by one hypothesis but not by its alternatives.")

---

[6] The complete testimony of three testifying experts in the *Peak & Collins* cases are attached for the Court's review. Dr. Eli Shapiro's testimony is attached as Exhibit K. Dr. Bruce Budowle's testimony is attached as Exhibit L. And, Dr. Ranajit Chakraborty's testimony is attached as Exhibit M.

[7] Forsensim and LoComatioN allow the user to specify drop-out and drop-in probabilities. *See* Exhibit D to Shapiro Decl., *FST Validation Study* at 750. Forensim then calculates the LR for a range of drop-out rates and displays the results graphically. *Id.; see also* Exhibit H, *Statistical Evaluation* at 378. LikeLTD finds the drop-out probabilities and mixtures that maximize the LR under the prosecution and defense hypotheses. *See* Exhibit D to Shapiro Decl., *FST Validation Study* at 750. TrueAllele uses electropherogram peak heights at every allelic position without taking drop-out into account. *See* Exhibit H, *Statistical Evaluation* at 379. And LabRetriever uses peak heights and allows the analyst to vary the drop-in and drop-out rates based upon the evidence. *See Rodriguez*, Sup Ct, NY County, Oct. 24, 2013, Caruthers, J., slip op. at 44-45.

Shockingly, despite its novel approach, the OCME never adequately tested its most critical assumption, i.e. that drop-out rates consistently correlate with DNA quantity. Dr. Adele Mitchell, one of the lead developers of the FST, testified that she: (1) never conducted a formal study to test the effect that changing the quantity of DNA could have on LRs; (2) did not publish her informal testing in any validation studies or other scientific articles; (3) never presented her testing to the DNA Subcommittee; and (4) did not show her work to anyone outside the OCME, or even to her supervisor inside the OCME. *See* Exhibit O, Testimony of Dr. Adele Mitchell, *People v. Peaks & Collins*, 5/21/13, at 28-32. In other words, Dr. Mitchell had insufficient evidence to support the most basic premise of the FST.

Correlating drop-out rates with DNA quantity was, thus, both idiosyncratic *and* unproven. Absent the performance and disclosure of studies documenting the validity of OCME's approach, the FST fails the testing requirement under *Daubert. See In re TMI Litig*, 193 F.3d 613, 674-75 (3d Cir. 1999) (holding expert testimony inadmissible because a crucial part of the analysis was a study that was never performed); *Daubert*, 509 U.S. at 593-95 (whether a theory or technique "can (and has been) tested" is a key factor bearing on reliability.) For this reason alone, the FST evidence should be excluded.

2. Using DNA Quantity to Determine Drop-Out is Prone to Error

The OCME's failure to test whether drop-out consistently correlates with DNA quantity is not the only problem with the FST. Dr. Theresa Caragine, another lead developer of the FST, has admitted that the OCME's method of quantifying DNA has a 30% error rate. *See* Exhibit P, Testimony of Dr. Theresa Caragine, *People v. Peaks & Collins*, 12/12/2012, at 41 ("The accuracy is within thirty percent of the expected value, which is much more accurate than

commercial tests.") Despite this admission, the OCME has not published any studies explaining how the error rate may affect the reliability of the FST. *See* Shapiro Decl. ¶ 38.

Moreover, while the OCME claims that its quantitation method is more accurate than that of the wider industry, it is not accurate enough for the purpose for which it was used in the FST. The accuracy of the quantification step of DNA analysis is appropriate for the purposes of optimizing the amplification step of traditional DNA typing because the amplification step tolerates a wide range of input DNA. It is also possible to discern from the electropherogram whether a sufficient quantity of DNA was used and to correct for possible error. *See* Exhibit K, Shapiro Test., 10/15/2013, at 183. But a 30% range of error is unacceptable for use in estimating drop-out rates because the FST comparison generates only *one* statistical value, and there are no opportunities to assess and correct any errors made during the process. *See* Shapiro Decl. ¶ 39.

In addition, within the framework of FST, there is no way to determine the proportion of each contributor's DNA to a DNA mixture. Thus, for DNA mixtures, the use of a single DNA quantity to estimate drop-out rates correlates little, if at all, with the drop-out rates for individual contributors. *Id*.

The OCME's failure identify (let alone even test) how the 30% error rate in quantitation impacts the LR compounds the uncertainty inherent in using quantity to determine the drop-out rate. Together, these failings undermine the program's reliability under two *Daubert* factors: (1) whether the methodology has been adequately tested, and (2) whether the actual relevant error rate is known. *See Daubert*, 509 U.S. at 594.

3. The OCME's Validation Studies Fail to Consider the Complex Features of Real-World Crime Scene Samples

On their face, the OCME's validation studies appear to rest on sound science. The OCME claims to have performed a large number of experiments; it has documented some of its findings; and it appears to have developed a tool consistent with those findings. But good and accepted science requires the rigorous testing and examination of assumptions and the willingness to perform additional studies and testing when initial assumptions are not borne out by the evidence or lack real-world application. The OCME falls far short of meeting these standards.

One of the most concerning features of the OCME validation studies is their failure to consider the unique features of real-world crime scene samples. The DNA samples the OCME examined in its validation studies were extracted from "pristine buccal swabs." Exhibit D to Shapiro Decl., *FST Validation Study* at 756.[8] ("The samples used for the current analysis were pristine buccal swabs.") By contrast, DNA extracted from evidence in the field is often degraded because of exposure to dirt, bacteria, or sunlight. Shapiro Decl. ¶ 23. Indeed, as discussed more fully below, the DNA extracted from the "thin sides of knife handle" in this case was heavily degraded.

In addition, the OCME assumed a very small number of possible mixture ratios for contributors to DNA samples. Ratios of 1:1 and 4:1 were used for two-person DNA mixtures; ratios of 1:1:1 and 5:1:1 were used for three person DNA mixtures. *See* Exhibit D to Shapiro Decl., *FST Validation Study* at 753. In the real world, however, the proportions of DNA each person contributes to a mixture are unknown and unlikely to conform to those derived from the

[8] Interestingly, OCME reports having tested 104 touched samples, but it does not report the results separately, nor does it present the drop rates or the false positive and false negative rates for touched items. *See* Exhibit D to Shapiro Decl., *FST Validation Study* at 752 (noting that 104 touch samples were used); Exhibit K, Shapiro Test., 10/4/13, at 72 ("They did not show in validation that I can see a curve or a graph or table that they show what were the likelihood ratios they obtained using degraded samples and what were the likelihood ratios using pristine values.")

validation studies. Shapiro Decl. ¶ 33; *see also* Exhibit K, Shapiro Test., 10/4/13, at 65 ("The actual ratios in the mixtures in real casework basically would almost never conform to those present models.")

Finally, the studies ignored the possible relatedness of the contributors to each other or the suspect, and the effect relatedness may have on allele drop-out. *See* Exhibit D to Shapiro Decl., *FST Validation Study* at 759 (the FST calculation is based on unrelated individuals). But relatedness is often an issue in real criminal cases. Related individuals commonly share touched items. And, of course, the possibility of relatedness is often a part of the defense hypothesis.

Importantly, the OCME acknowledges that degradation and relatedness may affect drop-out rates, and that further testing of these features is warranted. *See e.g.,* Exhibit D to Shapiro Decl., *FST Validation Study* at 756 ("The samples used for the current analysis were pristine buccal swabs. Results may differ if samples display[] more of the complicated characteristics of many evidence samples. Further study of these phenomena is warranted."); *Id.* at 759 (Further testing on degraded DNA samples is "warranted, as improvement in quantification of degradation or identification of moderately to severely degraded samples coupled with changes to the degradation model might improve performance."); *Id*. at 760 ("There are two main limitations to the current version of the FST application. First, correlation among genotypes of contributors to mixtures is not considered…"); Exhibit F to Shapiro Decl., *Perez Study* at 325 ("Consequently, touched items displayed a wider range of the number of different alleles than purposeful mixtures indicating that there was more allele drop-out and drop-in.")

In addition, scientific experts highly respected in the field of forensic DNA identification have criticized the OCME's failure to test and account for case-specific variables. Drs. Eli

Shapiro,[9] Bruce Budowle,[10] and Ranajit Chakraborty[11] are among the leading critics of the OCME's methodology. All three experts agree that degradation, mixture ratios, and relatedness can alter drop-out rates on a case-specific basis and thus affect the range of reasonable LRs. *See* Exhibit L, Budowle Test., 12/9/2013, at 822 ("The concept of using total DNA is – actually makes no sense...[because] we see from real casework the outcome is not consistent, it depends on the quality of the DNA, if it's degraded, if it's got inhibitors, these sorts of things."); Exhibit K, Shapiro Test., 10/4/13, at 64-65 ("Then when it's going to assign…a specific number of contributors to the mixture based on sort of preset criteria, without considering that there could be degradation, that there could be different numbers of contributors at different locations in the DNA but…larger and smaller locations….It doesn't…really count for all the different ratios of contributors that are possible and could be suggested by the actual evidence."); *see also* Exhibit B to Shapiro Decl., Peter Gill and Hinda Haned, *A new methodological framework to interpret Complex DNA profiles using likelihood ratios*, Forensic Sci. Int'l: Genetics 7, 251-263, at 262 (2013)(hereafter "*A new methodological framework*")("generalisation [sic] across the entire possible range of casework examples that may be encountered is unrealistic to achieve.

---

[9] Dr. Shapiro is a former assistant director at the Department of Forensic Biology at the OCME. He was the director of training there for roughly 10 years and leader of the Mitochondrial Team. He is a graduate of Columbia and Yale Universities.

[10] Dr. Budowle is a former senior scientist and lab head with the FBI, where his career spanned more than 25 years. His work was critical to developing the Combined Offender DNA Index. System (CODIS).

[11] Dr. Chakraborty is a professor in the Department of Molecular and Medical Genetics and the Director of the Center for Computational Genomics at the Institute of Applied Genetics at the University of North Texas Health Science at Fort Worth, Texas. He is a preeminent population geneticist. Dr. Chakraborty helped to develop the 13 core STR genetic markers used by the FBI and in labs throughout the world. Dr. Chakraborty was a member of the DNA subcommittee that approved the FST in 2010. Since voting for these methodologies, however, he has developed serious concerns about the use of the FST based on additional research and developments in the field, particularly in relation to complex cases.

Therefore the development of case-specific performance measures is needed to evaluate a likelihood ratio.")[12]

Despite the OCME's own admissions of weaknesses in the FST program, and the valid criticisms of leading experts, to this day, the OCME has not published any additional studies documenting how case-specific variables may affect the LR. And, to our knowledge, the OCME simply continues to use the pre-set rates, based on validation studies from pristine buccal swabs, with a minimal number of mixture ratios, and the DNA of unrelated individuals.

Features such as degradation, varying mixture ratios, and relatedness do not just impact the rare DNA case. One or more of these features is likely to impact *every* criminal case involving DNA mixtures. In fact, in this case, degradation is a significant problem with the sample that resulted in the LR of 4,070, with total drop-out occurring at 15 of the 30 loci. Since the effect of these features has never been validated, the LRs generated by the FST have no real-world application. They are unreliable and should be excluded under *Daubert. Cf. Reed Construction Data, Inc. v. The McGraw-Hill Cos., Inc.*, No. 09-CV-8578, 2014 WL 4746130, (SDNY Sept. 2014) ("to be admissible, a [statistical] regression analysis must control for the 'major factors' that might influence the dependent variable.") (citation omitted); *Medisim Ltd v. Bestmed LLC*, 861 F.Sup.2d 158, 166 (SDNY 2012) ("[T]he closer the survey methods mirror the situation in which the ordinary person would encounter the trademark, the greater the evidentiary weight of the survey results. The failure of a survey to approximate actual

[12] The current FST method of using pre-set criteria also fails to include a process for testing the false positive rate on a case-by-case basis. Leading scientists have rejected this approach, advocating for case-specific non-contributor performance testing to assess the weight of the evidence. *See e.g.*, Exhibit B to Shapiro Decl., *A New Methodological Framework* at 261 ("Interrogation with non-contributor performance tests…can be used to demonstrate the performance of the model. It is proposed here that performance tests also serve the purpose of validation on a per case basis…by providing a concurrent risk analysis. This flexibility is a desirable feature of any complex. theory, since it is impossible to generalize across the entire range of propositions/profiles that may be encountered.")

marketplace conditions can provide grounds for inadmissibility.") (citation and internal quotation marks omitted.)

4. The FST Assumes Independence of Drop-Out Rates Across Alleles Without Proper Validation

As part of its presentation to the DNA Subcommittee, the OCME submitted a summary of its validation studies as to the possible dependence of alleles across loci. In the summary, the OCME concluded that drop-out rates appear to be independent across loci. *See* Exhibit Q, Likelihood Ratio Statistics For Analysis of Single Source, Mixed and Degraded Evidence Samples, Volume 22: Determination of Independence of Drop-Out Among Loci, Summary at 1. ("Drop-out rates appear to be independent across loci. That is, drop-out or lack of drop-out at each locus is not consistently associated with an increased or decreased probability of drop-out at other loci."); Exhibit R, Declaration of Dr. Ranajit Chakraborty in *U.S. v. Rashawn Smalls* ("Chakraborty Decl."), ¶ 35. In other words, the OCME assumes that there is no correlation between drop-out at one locus and drop-out at other loci. *See* Exhibit R, Chakraborty Decl. ¶ 35. Dr. Chakraborty has examined the underlying data and has determined that it does not support this conclusion. *Id*.

First, the OCME disregards its own data. Attached to its summary conclusions, the OCME included tables reflecting the OCME's statistical analysis, which showed that some positive and negative correlations between drop-out rates at different loci were observed but were not consistent. *See* Exhibit Q, Summary at 3 ("Within each set of mixtures, drop-out at some loci was associated with drop-out (or lack of drop-out) at other loci. However, these associations were not consistent across the mixtures, indicating that there is no consistent correlation in drop-out probability among loci."); s*ee also* Exhibit R, Chakraborty Decl. ¶ 35.

Rather than trying to account for the complexities in the correlations or further studying them, the OCME reached a conclusion inconsistent with the data -- that the drop-out rate across loci is independent.

Second, the data set used by the OCME to reach its conclusion was limited and does not account for all of the real-life factors that could influence the dependence or independence of drop-out rates across loci; these include the varying number of contributors, allele sharing between them, varied mixtures ratios, and uneven degradation of the DNA. *See* Exhibit R, Chakraborty Dec. ¶ 36. Amazingly, OCME did not factor into its calculation of drop-out rates its failure to consider these variables. *Id*.

Third, the OCME's testing of drop-out across loci was too simplistic. *Id*. ¶ 37. OCME chose one locus, and asked whether drop-out rates there were consistent with drop-out at other loci under various conditions. *Id*. The OCME should have instead considered whether drop-out rates of all 15 loci were simultaneously independent of each other. *Id*.

Dr. Chakraborty has recommended that OCME complete further studies on the dependence of drop-out across loci. *Id*. at ¶ 38. To date, however, the OCME has not published any studies showing whether and/or how such additional work has been done or factored into the FST. *Id.* Perhaps neither further studies nor additional work have been done because the only laboratory to use FST has discontinued its use. Without an accurate assessment of the dependence/independence of drop-out rates, the LR ratios generated by the FST have no scientific value, and should be excluded under *Daubert.*

5. The Racial Identities of the Contributors to the Validation Studies Were Not Preserved, Making it Impossible to Verify Whether Racial Identity Was Properly Considered in Formulating Drop-Out Rates

In its validation studies, the OCME tested 439 mixtures. *See* Exhibit D to Shapiro Decl., *FST Validation Study* at 752 (noting that 454 mixtures and touched items were included in the validation, 15 of which were from only a single source.) The OCME's published validation studies described the racial background of contributors to the mixtures as follows:

> The 85 contributors represented the diverse population of New York City. For 72% of the samples, the ethnicity of the donor was known, as these donors were laboratory employees. The breakdown was as follows: 20% Asian, 16% Black, 54% Caucasian, and 10% Hispanic. The remaining samples were obtained at autopsy and represented a random draw from the population of New York City. According to the 2010 United States census, the population of New York City is 9.8% Asian, 26.6% black, 44.7% Caucasian, and 27% Hispanic.

Id. at 753.

Despite describing the racial composition of the contributors to the mixtures in its validation studies, the OCME did not preserve its data of the racial characteristics of the contributors for review and validation by other scientists. *See* Exhibit R, Chakraborty Decl. ¶ 40; *see also* Exhibit S, Testimony of Mimi Mairs, *People v. Peaks & Collins,* 6/17/13, at 9 (Mimi Mairs, Special Counsel, Forensic Biology at OCME stating in response to court's inquiry about availability of racial data underlying the FST study: "Doctor Mitchell states that she and, Doctor Carajine [sic] tallied up on a piece of scratch paper and that piece of scratch paper was not saved so when I say that there is no document much less a formal document, there is none.") Further, the OCME failed to provide to the DNA Subcommittee that approved the FST's use the data concerning the racial identifications or subpopulations of the contributors to the mixtures. *See* Exhibit R, Chakraborty Decl. ¶ 40.

Racial and subpopulation characteristics are critical to an accurate determination of drop-out rates, and this data should have been preserved for external review. Dr. Chakraborty has explained that allele frequency is an important possible predictor of drop-out rate, and allele frequency varies by race and ethnicity, with members of the same race and ethnicity sharing more alleles. *See* Exhibit R, Chakraborty Decl. ¶ 39; Exhibit M, Chakraborty Test., 12/16/13 at 1119-20; *see also* Exhibit L, Budowle Test., 12/10/2013, at 921 ("[I]f you take two people who are Caucasians, they are more likely to share alleles amongst them, just being Caucasians….If you take two Africans, they have a better chance of sharing two alleles in common because they have certain ones more common. So, you get -- it would be different alleles that are more common in one population than another.") In Dr. Chakraborty's expert opinion, if race and ethnicity are not properly accounted for, the drop-out rates will be unreliable. *See* Exhibit R, Chakraborty Decl. at ¶ 39.[13]

The lack of transparency of the manner in which race and subpopulations factored in the drop-out rate materially undermines the reliability of the FST under at least two *Daubert* factors: (1) whether the theory or technique has been tested and subjected to peer review, and (2) whether it has a known rate of error.

B.

The Likelihood Ratios Generated by FST Often Prejudice the Defense

One effect of correlating drop-out with DNA quantity is that there is no opportunity to propose alternative assumptions for the prosecution and defense hypotheses. There is only one

[13] Dr. Chakraborty has also explained that racial identification of the contributors to mixtures would be important in assessing the false positive rate. *See* Exhibit M, Chakraborty Test., 12/16/13, at 1120. Therefore, the absence of racial identification data also calls into question the reliability of OCME's assessment of the appropriate false positive rate.

drop-out rate, and it is held constant between the hypothesis that the defendant was involved and the hypothesis that he was not. *See* Exhibit D to Shapiro Decl., *FST Validation Study* at 757 ("[W]e elected to empirically estimate drop-out rates as a function of the total amount of template DNA in a sample, the estimated number of contributors to the sample, their approximate ratio (equal or not equal) and STR locus.") While the OCME argues that this approach is "conservative," the truth is that this method can and does increase the LR in certain cases. *Id.* at 752.

OCME purports to adjust for potential prejudice to the defense by intentionally underestimating the drop-out rate and assuming the minimum number of contributors to a sample. *Id*. at 752 ("In order to be conservative, FST uses the drop-out rate estimate minus one standard deviation for each locus, template DNA quantity, number of contributors, and ratio for mixed samples.") Neither adjustment, however, has the desired effect.

1. Holding the Drop-Out Rate Constant Can Prejudice the Defense

Other developers of drop models allow for varying the drop-out rate between the numerator and the denominator. Hinda Haned and Peter Gill, for example, have developed an exploratory model that allows the application of different drop-out probabilities to different contributors, and the use of different parameters under the prosecution and defense hypotheses. In a 2012 article discussing their model, Haned and Gill explained that "varying the probabilities of drop-out between the two hypotheses, *Hp* and *Hd,* led to dramatic changes in the LRs. This shows that the chosen values for the probabilities of drop-out are a very critical part of the implementation of the model in casework." Exhibit J, *Exploratory data analysis* at 773.

One reason Haned and Gill consider variation in the drop-out rate as critical to their model is that holding the rate constant can prejudice the defense. During his testimony at the *Peaks/Collins Frye* hearing, Dr. Budowle demonstrated that maintaining the same drop-out rate in both the numerator and denominator generated a higher LR at least some of the time. Moreover, increasing the drop-out rate in the denominator often lowered the LR. *See* Exhibit L, Budowle Test., 12/9/2013, at 830-31 ("[T]here is a point…as you lower the drop-out rate, [the LR is] eventually going to get low but there is a certain sweet point where it will be higher. If the drop-out is higher it will be a sweet point and give a more conservative value. There is a certain point where it's very high, it will go in the opposite direction. So, it all depends on a case by case basis what the effect is.")

Given the potential prejudicial effect of holding the drop-out rate constant, Dr. Budowle advised: "[I]f the prosecution forms and controls the conditions for the prosecution's hypothesis, the defense should be able to form at least reasonable hypotheses based on what the evidence is on the validation studies. So if you can't adjust the drop-in and drop-out rates based on data, then that's not an appropriate thing to do." *Id*. at 912; s*ee also* Exhibit B to Shapiro Decl., *A New Methodological Framework* at 261 (noting that a necessary feature of any LR model is that it "must be able to determine numeric strength of evidence that favours defense or prosecution hypotheses.")

2. <u>There is No Empirical Evidence that Underestimating the Drop-Out Rate is Conservative</u>

The OCME purports to adjust for any potential prejudice that results from holding the drop-out rate constant by intentionally underestimating the drop-out rate. But nowhere does the OCME demonstrate how or why this works. Dr. Mitchell testified during the *Peaks/Collins Frye*

hearing that she never conducted a formal study on the underestimation of drop-out rates, but instead tested the proposition informally "on my own." Exhibit O, Dr. Mitchell Test., 5/1/13, at 117. She further acknowledged that she did not publish the results and does not know whether she even saved them. *Id.* And perhaps most troubling, the results of her informal testing were not communicated to the DNA Subcommittee. *See* Exhibit R, Chakraborty Decl. ¶ 43.

Dr. Chakraborty tackled this issue head-on: he examined the available data, and determined that it does not support the OCME's assumption. Indeed, his review of the OCME's "Study 3C" shows that underestimating drop-out rates leads to a lower LR only half the time. *Id.* at ¶ 43. As Dr. Chakraborty put it during his testimony at the *Peaks/Collins Frye* hearing, underestimating drop-out "is as good as tossing a coin." *See* Exhibit M, Testimony of Dr. Ranajit Chakraborty, 12/16/2013, at 1127. Half the time it will favor the prosecution.

The OCME's failure to formally test its assumption, and Dr. Chakraborty's expert critique, both undermine the reliability of the FST methodology under *Daubert.*

3. Assuming the Minimum Number of Contributors Prejudices the Defense

The OCME admits that "precise accuracy rates for estimating the number of contributors cannot be calculated." Exhibit F to Shapiro Decl., *Perez Study* at 324. It, thus, assumes the minimum number of contributors to a sample, which it also claims produces the lowest LR. *Id.* at 315 ("In other words, for a given prosecution hypothesis, using the defense hypothesis with the minimum number of possible contributors will usually result in the lowest possible LR…."); *see also* Exhibit D to Shapiro Decl., *FST Validation Study* at 759 ("using the minimum number of contributors typically results in the lowest possible LR, the LR that most favors the defendant.")

But this disregards the substantial risk that underestimating the number of contributors will actually increase the LR, prejudicing the defense. Even the OCME acknowledges "a 'moderate risk' of a non-minimal LR when the defense hypothesis with the minimum number of contributors is used." Exhibit F to Shapiro Decl., *Perez Study* at 316. Moreover, leading scientific experts have shown that underestimating the number of contributors can result in higher LRs in a significant number of cases. For instance, in *A New Methodological Framework*, Gill and Haned presented a case study involving two suspects of a sexual assault, both of whom denied the offense. *See* Exhibit B to Shapiro Decl., *A New Methodological Framework* at 255-256. When the mixture was treated as having only two contributors, the LR for one of the suspects was much higher than if three contributors had been assumed. *See id*. at 256. Thus, the choice of three contributors over two was "demonstrably conservative." *Id*.

Experts have further shown that the risk of higher LRs increases as the number of contributors to a DNA mixture increases. *See* Exhibit C to Shapiro Decl., *Complex. DNA mixture analysis* at 22 (In tests performed, underestimating the number of contributors led to more conservative LRs in 85% of three-person samples, 56% of four-person samples, and 49% of five-person samples.) Thus, the greater the number of contributors to a sample, the greater the possibility that underestimating the number will prejudice the defense. *See* Shapiro Decl. ¶ 31. This, too, undermines the reliability of the FST model under *Daubert.*

In short, whatever the purported merit of using quantity to estimate pre-set drop-out rates, the FST's system of fixed parameters often results in a higher LR, thereby prejudicing the defendant. Because this methodology is not generally accepted in the scientific community, the results of the FST should be excluded under *Daubert.*

C.

The Publication of the Source Code Further Undermined the Reliability of FST

Obscured until the source code was made available for review in *United States v. Kevin Johnson*, was just how deceptive the entirety of FST's putative validation was, its supposed review before the New York State Forensic Science DNA Subcommittee, the two articles by its authors and designers, and the whole of two admissibility hearings pursuant to *Frye v. United States*, 293 F. 1013 (D.C. Cir. 1923). Countless representations have been made as to FST's transparency, its reproducibility, and its lack of bias. But the review of the code that was conducted in *Johnson* showed precisely the opposite.

1. Undisclosed behaviors

Now that an initial review of the FST source code has been conducted, it has come to light that the program in fact performs LR calculations subject to a formula that has never been reported, and which can favor the prosecutor's hypothesis.[14] Explained below, the embedded code jettisons data for entire loci when the sum of the frequency of individual alleles seen at those loci is considered to be unacceptably high (0.97 or higher). A high total allele frequency means most random individuals would be included in the mixture. As FST is supposed to calculate the potential frequencies for every possible genetic combination at each locus, eliminating a locus entirely where most genotypes are included is likely to favor the government. Additionally, as previously noted, DNA statistical results lose discriminatory power when loci are dropped, and increase false positive associations.

[14] *See* Exhibit T, October 27, 2016 Declaration of Nathan Adams in *U.S. v. Johnson* (15-CR-565) ("Adams 2016 Decl.") at section 5.6; *see also* Exhibit U, February 12, 2017 Declaration of Nathan Adams in *U.S. v. Johnson* (15-CR-565) ("Adams 2017 Decl."), section 3.5. (Adams is also one of Mr. Sherland's anticipated Experts).

This powerful, highly influential feature of FST has never been reported anywhere and was revealed only during the review of the source code. It is axiomatic that it has never been subjected to even minimal peer review. To the contrary, indications are that strenuous effort has been expended to prevent it.

Nowhere in any of the FST documentation – the testimony to the DNA subcommittee, the published papers, the lab validation studies, the state court *Frye* hearing transcripts, all state and federal court trial testimony on FST, the affidavits from Dr. Mitchell or Dr. Craig O'Connor in federal cases, webinar presentations to the forensic community on FST, etc. – is there any indication that this data-discarding function existed, or was part of the FST methodology.

In fact, there is little indication that anyone at the OCME even knew of the data-discarding function, other than the individual who coded it into the FST. In other words, the operator doesn't record this phenomenon; nor is it included in a subject's FST results.[15] It is a function of the software that was previously undetected.

Performance checks of the FST that compared LR before and after the data-discarding function was brought online for casework showed that dropping loci could be prejudicial to a defendant. The modified FST was brought online anyway.[16]

2. Flawed Software Engineering

Nathan Adams explains the importance of testing software "on its own, in accordance with strictly defined test criteria developed from its own requirements and specifications

[15] *See* Exhibit T, Adams 2016 Decl., section 5.6; *see also* Exhibit U, Adams 2017 decl., section 4.

[16] *See id*.

documents."[17] "Using IEEE's definition of verification, '[t]he process of evaluating a system or component to determine whether the products of a given development phase satisfy the conditions imposed at the start of that phase,' it is difficult to assess what verification processes have been undertaken during FST's validation and continued use."[18] No explicit protocols have been provided.[19] The FDA further recommends that software testing be performed independently, i.e. "performed by an organization free from control by the supplier, developer, operator, or maintainer."[20] That was clearly not done with the FST.

The stylistic conventions of code do not follow one style guide.[21] No specific style guide was included in the validation study, nor in any other material that Mr. Adams was provided in *Johnson*.[22] The risk caused by this absence is this: "Without explicit descriptions of intended behaviors, reviewers and developers are left to infer the purpose of the code from its own function. In the absence of external definitions of intended functionality, a developer runs the risk of justifying the behavior of existing code by its sheer existence."[23] Style guides help prevent "code smells" – "a smell is not a defect in itself but is a deviation from good coding practices, which can indicate underlying software defects."[24] Adams found smells throughout the FST code.

---

[17] *See* Exhibit T, Adams 2016 Decl., section 5.2.2.

[18] *Id*. at 5.3.

[19] *Id*. at 5.3.1.

[20] *Id*. at 5.3.2.

[21] *Id*. at 5.4.3.1.

[22] *Id*.

[23] *Id*.

[24] *Id*. at 5.4.3.2.

Adams also found instances in the FST code where the function of the code itself was, at best, mislabeled. At worst, it didn't work. For example, in one comparison dropdown list, options #3 and # 4 could be activated only if, instead, Adams selected #5 and #6. In other words, the program required choosing one option in name to perform another option's function.

The inconsistencies that Adams found between the validation study's description of the code's behaviors and the source code demonstrated for the first time that this version of the FST is not the same program that was validated by the OCME. This lends further support for the conclusion that evidence derived from the FST should not be admitted against a criminal defendant at a trial.

D.

The FST Has Not Been Subjected to Adequate Peer Review

As discussed above, scientific experts cannot adequately test the validity of the FST because the OCME refuses to disclose critical studies in support of its most fundamental assumptions. The missing, or non-existent, studies include: (1) studies testing whether drop-out rates consistently correlate with DNA quantity, (2) studies testing how the 30% error rate in quantitation affects the LR, (3) studies testing how the unique features of real-world crime scene samples affect drop-out rates and the LR, (4) studies testing whether the drop-out rate across loci is dependent or independent, and (5) studies testing how underestimation of the drop-out rate affects the LR. Should these studies in fact exist, this Court should order the government to obtain and turn them over to Mr. Sherland and produce them at a *Daubert* Hearing (if one is ordered).

District Court Judge Brian M. Cogan of the Eastern District of New York, in *U.S. v. Rashawn Smalls*, commented about FST in this regard:

> Well, that gets me to the broader concern I have with FST, which is when you're dealing with a scientific testing protocol, it's a different kind of peer review to sit down with a body of peers and say here's what we've done and here's what we found and have all the peers say, well, what you say is logical, it makes sense, we find no fault in it and we, therefore, approve it. That's one kind of peer review. The other kind of peer review that [I] think is most important, not necessarily required under *Daubert* but most important in the area of scientific testing, is replication; that is, here's our source code, you do it, you test our assumptions, you see if it comes out the same way. And that hasn't been done.

Exhibit V, Transcript in *U.S. v. Rashawn Smalls* (14-CR-414), June 25, 2015, Hon. Brian M. Cogan, Eastern District of New York.

Judge Cogan's commentary is even more cogent now that we know that the FST that OCME sat down with the DNA Subcommittee and said here's what we've done, and here's what we've found, is not the FST that they've been operating for years, unbeknownst to anyone outside of the OCME; nor is it the FST used to produce the results the government intends to offer at trial against Mr. Sherland. None of the newly discovered information concerning changes to the FST has been vetted by experts outside those on the OCME's own staff. This is troubling and seriously undermines the reliability of FST under *Daubert.*

And, while the source code was published online five months ago, ostensibly giving the scientific community an opportunity to test the reliability of the FST program it has raised more questions than it has answered. Further, as mentioned earlier, because the code was published well after the OCME stopped using the FST on January 1, 2017, and the OCME was the *only* lab in the world using the FST, there is a reduced interest in the scientific community in deciding whether the FST works. Even apart from that, much of the key data used to develop the FST has not been preserved and/or made available for inspection by the scientific community. These

flaws further render the FST unreliable under *Daubert. See Daubert*, 509 U.S. at 594 ("'a known technique which has been able to attract only minimal support within the community' may be properly viewed with skepticism") (quoting *United States v. Downing*, 753 F.2d 1224, 1238 (3d Cir. 1985)).

E.

The FST Is Unreliable and Prejudicial When Applied to the Specific Facts of this Case

In addition to making a determination regarding the independent reliability of a scientific methodology, courts also must examine reliability "in light of the particular facts of the particular case." *Kumho Tire Co., Ltd.*, 526 U.S. at 158. The sheer power associated with scientific evidence—especially DNA evidence—warrants the Court's careful review of the testing performed in this case. *See Daubert*, 508 U.S. at 595 ("Expert evidence can be both powerful and quite misleading….Because of this risk, the judge in weighing possible prejudice ...exercises more control over experts than over lay witnesses.") (citation omitted).

(1) Swab "RB/S2" from "thin sides of knife handle"

The sample from "thin sides of knife handle," which when compared with Mr. Sherland's DNA profile yields a LR of 4,070, is severely degraded. Degraded samples by their very nature supply less information, making them less probative. This sample yields total dropout at 15 of the 30 loci.

Profile	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317
Dominick Sherland	12, 15	31.2, 32.2	10, 11	11, 11	16, 17	7, 8	11, 13
Evidence							
Run 1	12, 13, 14, 15				14, 15, 16, 17	6, 7, 8	
Run 2	12, 13,	31.2			14, 15,	6, 7, 8,	11

	14, 15				16, 17	9.3	
Profile	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
Dominick Sherland	9, 9	22, 23	12, 13	14, 16	6, 8	13, 17	11, 13	21, 25
Evidence								
Run 1			12, 13	16				
Run 2	9		11, 12, 12.2, 13, 14, 16	14, 15, 16, 18, 20	6, 8		11, 12, 13	

Based on a DNA template amount of 115 picograms, FST calculates the dropout rate at each locus to be 5%. *See* Exhibit E to Shapiro Decl. Yet this sample has at least 50% total dropout rate. Such a drastic difference in the actual drop rate and FST's predetermined drop-out rate can have significant affects on the LR, which could prejudice Mr. Sherland. *See* Shapiro Decl. ¶ 44. In particular, where the FST doesn't give us a locus by locus LR, and we don't know how the FST apportions the LR between loci, it's impossible for us to know exactly how the total drop-out rate alters the LR produced by the FST. *Id*. Further, in light of the fact that the FST was tested only using pristine buccal swabs, and its creators have as much as admitted that further testing is warranted on degraded samples (*see* Exhibit D to Shapiro Decl., *FST Validation Study* at 759), significant questions of reliability are necessarily raised about the results of the FST on this highly degraded sample. *See* Shapiro Decl. at ¶ 45.

In addition, there are only four loci where Mr. Sherland's alleles show up in both runs. Approximately 18% of the population, or 1 in 5 people, are included at those four loci. The weak discrimination power of these four loci should be recognized in analyzing the strength of this evidence. Further, because the FST does not return a locus by locus summary of its results, it is not possible to confirm how much of the reported total LR of 4,070 is based on non-reproducible loci, where Mr. Sherland's alleles are missing from both runs.

Lastly, while the OCME reports its results in a way that includes a reference to a specific number of persons in a mixture (Mr. Sherland + 2 unknown persons vs. 3 unknown persons), the calculation of the number of contributors can be an arbitrary determination subject to known uncertainty. Here the OCME has concluded that the sample from the "thin sides of knife handle" was a three-person mixture. However, the total allele count is 31, which could also support a two-person mixture. *See* Shapiro Decl. ¶ 46. In the *Perez Study*, the minimum number of alleles seen in 184 known two-person mixtures was 35. *See* Exhibit F to Shapiro Decl. (Table 3). The recommended minimum allele count for a three-person mixture is 47. *See id*. (Table 5). The sample in this case only exhibited one of the nine criteria listed for a three-person mixture in Table 2. *See id*. (Table 2). Especially where there are only two loci with more than four alleles, the additional alleles could be accounted for by drop-in instead of a third contributor. *See* Shapiro Decl. ¶ 46. Alternatively, given the fact that there are more than four alleles at D19S433 and vWA, and because the sample is so degraded, it's equally possible that it could have been a four person mixture just with more dropout. *Id*. at ¶ 47. Figure 5 of the Perez Study shows that 6 out of 36 (16%) of known 4-person touch DNA mixtures showed fewer than 31 alleles when analyzed. *See* Exhibit F to Shapiro Decl. Mischaracterization of a 4-person mixture as a 3-person mixture would be significant because FST is not validated for 4-person mixtures. *See* Shapiro Decl. ¶ 47. Whether two or four, any change in the number of contributors would have a significant effect on the LR. *Id*. at ¶ 48.

Therefore, the inherent uncertainty here tends to further undermine the FST as it is applied to this sample.

(2) Sample from handle of knife

The sample from the handle of the knife, which when compared with Mr. Sherland's DNA profile yields a LR of 4.59.

Profile	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317
Dominick Sherland	12, 15	31.2, 32.2	10, 11	11, 11	16, 17	7, 8	11, 13
Evidence							
Run 1	12, 14, 15, 16	29, 31, 32.2, 37	8, 10	11, 12	14, 15, 16, 17	6, 7, 8, 9.3	11, 12, 13
Run 2	12, 13, 14, 15	27, 29, 37	8, 10	11, 12	14, 15, 16, 17	6, 7, 8	11, 12, 13

Profile	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
Dominick Sherland	9, 9	22, 23	12, 13	14, 16	6, 8	13, 17	11, 13	21, 25
Evidence								
Run 1	8, 9, 11, 12, 13	17, 23	11, 12, 12.2, 13, 14, 15	14, 15, 16, 18, 20	6, 8, 9	13, 16, 17	11, 12, 13	21, 24
Run 2	9, 10, 11, 12	17, 22	11, 12, 12.2, 13, 14	14, 16, 17, 20	6, 8		11, 12, 13	19, 24

The same uncertainties that were described for the previous sample apply to the FST calculations here, rendering the reported LR unreliable. *See* Shapiro Decl. ¶ 51. In this sample, it is also important to emphasize that the uncertainties in the allele frequencies that FST uses, render the LR of 4 indistinguishable from a LR of 1, which is inconclusive. *Id.* It is prejudicial to assert *even limited* support for the prosecution hypothesis for LR values below 10, when the LR is based on population genotype estimates that are known to vary 10-fold above and below the calculated value even within the same sub-population. *Id.* This concern, that OCME wildly

overstates the precision of the FST calculation, does not even factor in all the other estimations and approximations that make up the FST parameters. *Id*.

CONCLUSION

The FST is unreliable both independently and as applied to the facts of this case. The FST was never generally accepted in the scientific community as OCME was the *only* laboratory in the world to ever use it, and not even the OCME is using it anymore. The FST's unique system of fixed parameters fails to account for the specific features of real world crime-scene samples, including those which are clearly present in Mr. Sherland's case, and can have the effect of making the LR higher, which prejudices the defense. The source code has shown that the FST performs differently than was described by its creators, which has clear implications for the reliability of the FST. Plus, the FST as it currently exists has never been vetted by any expert outside of the OCME; it has simply not been subjected to adequate peer review.

Any of one these issues should bar the admission into evidence at trial of any results of the FST, as the LR is uniquely open to bias and unfair prejudice. The FST's record reflects a disregard of sound methodology so complete as to undermine even the relevance of the FST's results. Admitting the results here against Mr. Sherland would violate the *Daubert* standard, Mr. Sherland's rights under the Fifth, Sixth and Fourteenth Amendments, and FRE 702 and 403.

For all of these reasons and any other that the Court finds appropriate, we seek the exclusion of all DNA evidence generated by, and testimony concerning, FST, or in the alternative, we ask that the Court hold a *Daubert* hearing.

Respectfully submitted,

Edward V. Sapone
Edward V. Sapone